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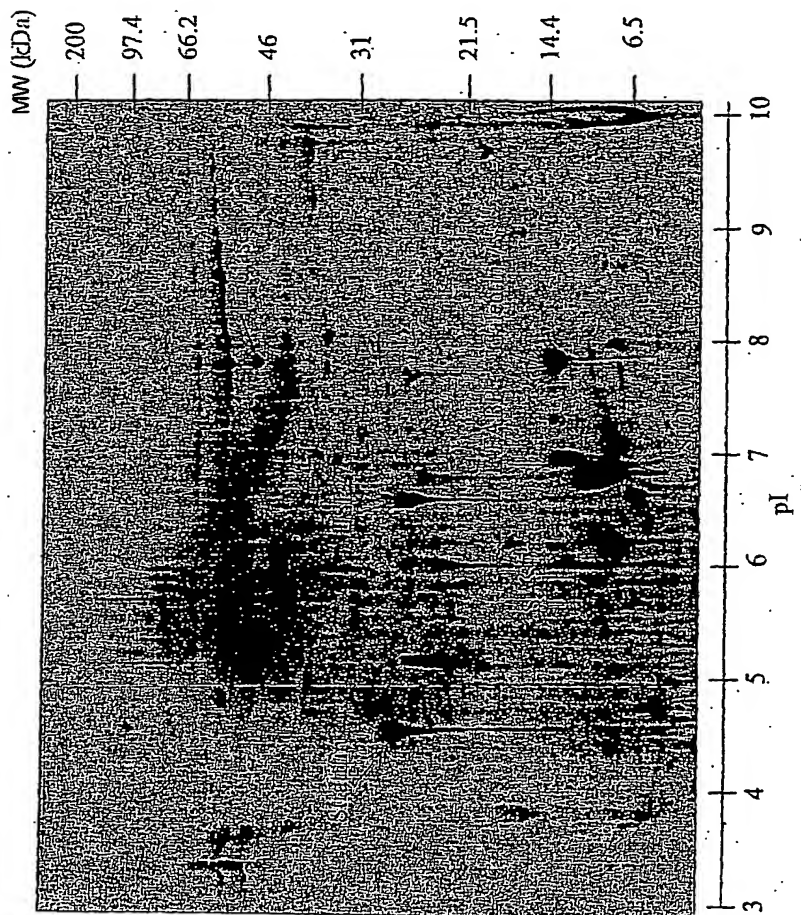


Figure 1

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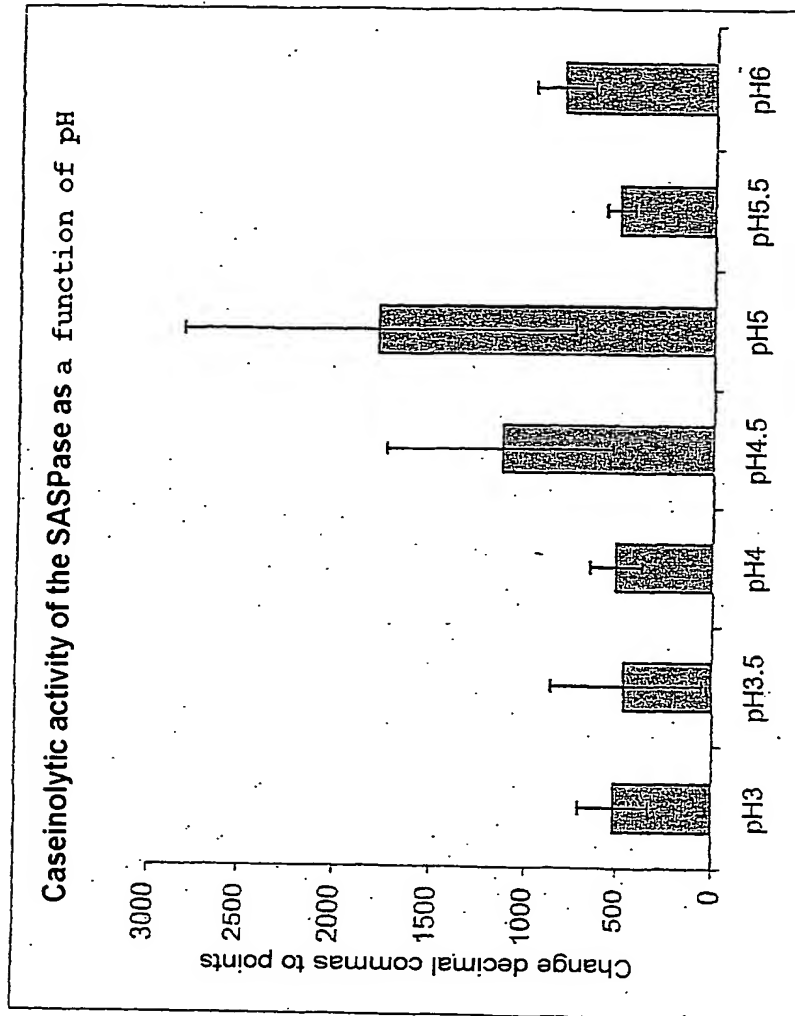


Figure 2

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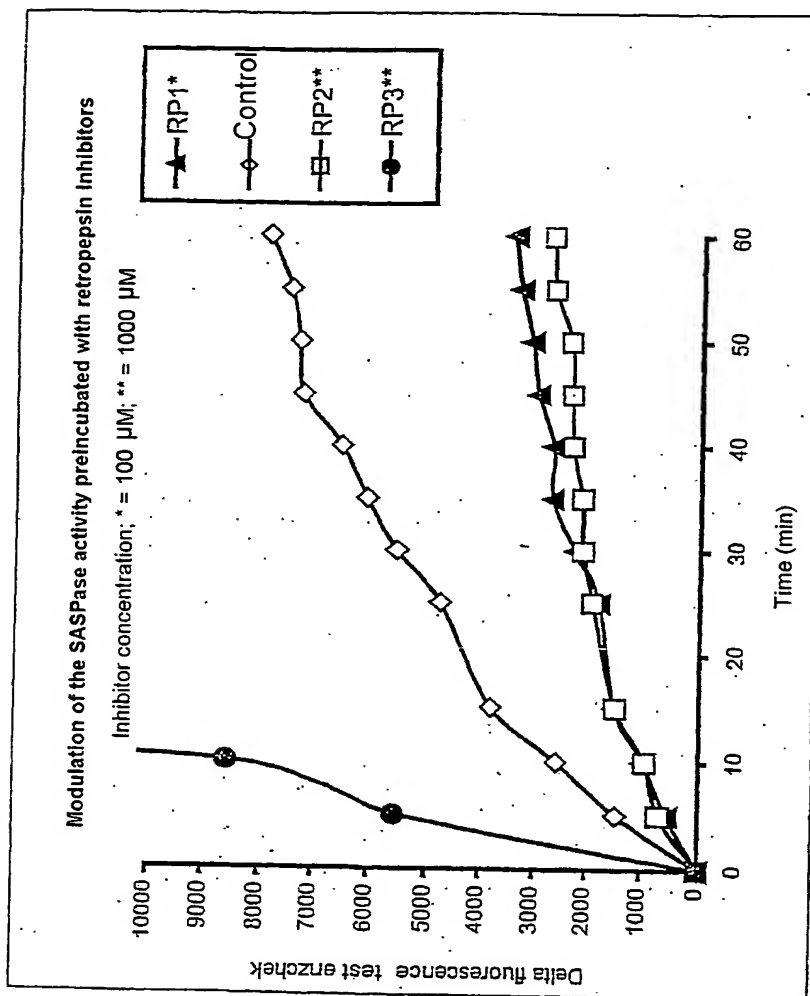


Figure 3

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CLUSTAL W (1.81) multiple sequence alignment

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      FIAV          IGFVNYNKKVGTTTLEKRP ELLIFVNGYPIKFLLDTGADITILNRRDFQVKN-----SIE 55
      HIV2          -----PQFSLWKRPPVVTAYIEGQPV ELLDTGADDSIVAG--IELGN-----NYS 43
      SASPase       -----ANSMGKGYLYLKGKIGKVPVRFLVD SGAQVSVVHPNLWEEVTDGDLDTLQ 49
                  :: * : : : * : * : * : * : * : * : * : * : * : * : * : * :
      FIAV          NGRQNMIG-VGGGKRGTNYINVHLEIRDENYKTQCIFGNVCVLEDN SLIQPLLGRDNMIK 114
      HIV2          ----PKIVGGIGGFINTKEYKNVEIEV LNKKVRA TIMTG-----DTPIN-IFGRN ILTA 92
      SASPase       PFENVVKVANGAEMKILGVWD TAVSLGKLKKAQFLVAN-----ASAE EAIIGTDVLQD 103
                  : . * . . : . : . : . : . : . : . : . : . : . : . : . : . :
      FIAV          FNIRLVMAQ-----123
      HIV2          LGMSLNL-----99
      SASPase       HNAILDFEHRCT LKGGKFRLLPVGGSLEDEFDLE 138
                  . * :
  
```

Figure 4

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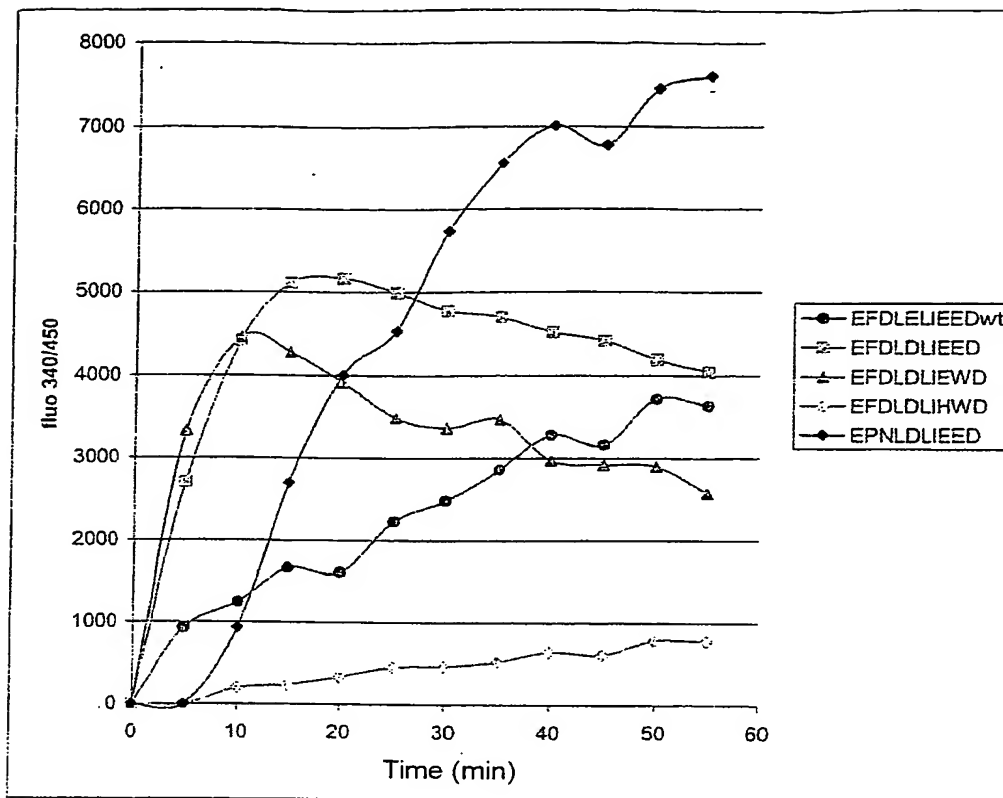


Figure 5